09/966,459
1 of 12

FIG. 1

ATGATGGTGGATCCCAATGGCAATGAATCCAGTGCTACATACTTCATCCTAATAGGCCTC
CCTGGTTTAGAAGAGGCTCAGTTCTGGTTGGCCTTCCCATTGTGCTCCCTCTACCTTATT
GCTGTGCTAGGTAACTTGACAATCATCTACATTGTGCGGACTGAGCACAGCCTGCATGAG
CCCATGTATATATTTCTTTGCATGCTTTCAGGCATTGACATCCTCATCTCCACCTCATCC
ATGCCCAAAATGCTGGCCATCTTCTGGTTCAATTCCACTACCATCCAGTTTGATGCTTGT
CTGCTACAGATGTTTGCCATCCACTCCTTATCTGGCATGGAATCCACAGTGCTGCTGGCC
ATGGCTTTTGACCGCTATGTGGCCATCTGTCACCCACTGCGCCATGCCACAGTACTTACG
TTGCCTCGTGTCACCAAAATTGGTGTGGCTGCTGTGGTGCGGGGGGCTGCACTGATGGCA
CCCCTTCCTGTCTTCATCAAGCAGCTGCCCTTCTGCCGCTCCAATATCCTTTCCCATTCC
TACTGCCTACACCAAGATGTCATGAAGCTGGCCTGTGATGATATCCGGGTCAATGTCGTC
TATGGCCTTATCGTCATCATCTCCGCCATTGGCCTGGACTCACTTCTCATCTCCTTCTCA
TATCTGCTTATTCTTAAGACTGTGTTGGGCTTGACACGTGAAGCCCAGGCCAAGGCATTT
GGCACTTGCGTCTCTCATGTGTGTGCTGTGTTCATATTCTATGTACCTTTCATTGGATTG
TCCATGGTGCATCGCTTTAGCAAGCGGCGTGACTCTCCGCTGCCCGTCATCTTGGCCAAT
ATCTATCTGCTGGTTCCTCCTGTGCTCAACCCAATTGTCTATGGAGTGAAGACAAAGGAG
ATTCGACAGCGCATCCTTCGACTTTTCCATGTGGCCACACACGCTTCAGAGCCCTAG

FIG. 2

MMVDPNGNESSATYFILIGLPGLEEAQFWLAFPLCSLYLIAVLGNLTIIYIVRTEHSLHE
PMYIFLCMLSGIDILISTSSMPKMLAIFWFNSTTIQFDACLLQMFAIHSLSGMESTVLLA
MAFDRYVAICHPLRHATVLTLPRVTKIGVAAVVRGAALMAPLPVFIKQLPFCRSNILSHS
YCLHQDVMKLACDDIRVNVVYGLIVIISAIGLDSLLISFSYLLILKTVLGLTREAQAKAF
GTCVSHVCAVFIFYVPFIGLSMVHRFSKRRDSPLPVILANIYLLVPPVLNPIVYGVKTKE
IRQRILRLFHVATHASEP

FIG. 3

CCACGCGTCCGCTCTGCCCTGAATCCAGGATAGACCAGGACAACAAGATGAGTGGCTAAC
TGTAGGATGGTGTCCATCTGTGCTCTAGGGGAGGAGTAGCATCAAAGGAGAAGCAAGAAC
TGAGAACTGTTTGGGGCACTGAAGAAGTAGGACTAAGGAAGAGTTAGGGGGTTAGTACAA
ATCTGAGGCCTGGTTTTCTGGAAAGAGACCAGAGACTGACCTTATTGCATGTCATACAAC
ATGCTTGCTTAGAGACCCCTAATTTATTTTCTTCTCTTACTCTTTCTGAGGAAGCATGAG
CCACACCCTCAGTTAGTTTTGTATAATCTTAGGCTTGATGAGAATATAATCTTAGTCTTG
AAGGCTTTAAAGGGGAAGAAATAGCTGTCTGTGTTAGTGGTGTGTCAGTCAGCAGGAGAA
CCTGCTAGGGGTGGAAGGAGGAGGGTAGGAGTATAGCCTAGACCATGAGTAGATACCCCG
CTCCACCTTGAAAGTCTCCTACTGGACCTCTTATGATGGAGTTAATACCTCCTGTTTCCT
CTATTCCAGATTGTTTTCAGTTTCCAGAAGGCAAAACTGACATCTCCCAGGAGTCCAAGT
AGGAGATTAGGGCCTCCCGTCCCTATCTACTCAGTGCTAGCCTTGGCTAAGAGAGAGGAA
ATTCCTGCCTAGAGGGGAAAATCTGCAGGACTTCGTTACCACTTTCACTTTGGCAGAGGA
AGGAGGTCAGGGATGGAAGGGGAAGTGAGTCTAGAAATTAAAACATAGAATTCTGTCTAC
AGGTGGTGGAGAGCCTTTCTGAAAGTGCTTCTGGGTTGAGGCTGTCACCTAGATTTTATA
TTAGAGTTTAAGTGTTCCAAAAAATTAAGAAGCAGGAAGTAGAAAAGAGAACAATTTCAG
AAGCAGACGAAAGGAACAGTAATAGGAAGATCTAGCAAGGATGTGGTGGGGCAGTTTCAG
TGTGAGATGCCATGGACAGGAAAATGGCAGCATATGTGTGTGTGTGTGTGTGTGTGTGTG
TCCATGAGACAGAGAGACATAAATAACTAAATAAAAAGGCATATCACAAAGAGGGGCTCC
TGCTTCAGCTTGAGTCCTGGATGCAAAGACATGTGGACTGGGATCCTAGCAACCTATCTG
CAGCCAAGGACATGACGTTAGACGCCCCAAGAAAAGGAAAATTGGTCAAACATAGGAAGA
GCACTCAAGTGCCAGCTACAGTGAATGACAAATACCCACCACAAGCACAAGCTCTACATT
CACAAAAACTTGGAAAACACAAGTTCATAGACTGGGCAACCCTGAGTAGTGGAGAGATCA
CCAGCCATGTTTCAGGTTGTACCCTCTACCTGCCTGGTGCTGGTCACAGTTCAGCTTCTT
C

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FIG. 4

GTGTCAGTGATCAAACTTCTTTTCCATTCAGAGTCCTCTGATTCAGATTTTAATGTTAAC
ATTTTGGAAGACAGTATTCAGAAAAAAAATTTCCTTAATAAAAATACAACTCAGATCCTT
CAAATATGAAACTGGTTGGGGAATCTCCATTTTTTCAATATTATTTTCTTCTTTGTTTTC
TTGCTACATATAATTATTAATACCCTGACTAGGTTGTGGTTGGAGGGTTATTACTTTTCA
TTTTACCATGCAGTCCAAATCTAAACTGCTTCTACTGATGGTTTACAGCATTCTGAGATA
AGAATGGTACATCTAGAGAACATTTGCCAAAGGCCTAAGCACGGCAAAGGAAAATAAACA
CAGAATATAATAAAATGAGATAATCTAGCTTAAAACTATAACTTCCTCTTCAGAACTCCC
AACCACATTGGATCTCAGAAAAATACTGTCTTCAAAATGACTTCTACAGAGAAGAAATAA
TTTTTCCTCTGGACACTAGCACTTAAGGGGAAGATTGGAAGTAAAGCCTTGAAAAGAGTA
CATTTACCTACGTTAATGAAAGTTGACACACTGTTCTGAGAGTTTTCACAGCATATGGAC
CCTGTTTTTCCTATTTAATTTTCTTATCAACCCTTTAATTAGGCAAAGATATTATTAGTA
CCCTCATTGTAGCCATGGGAAAATTGATGTTCAGTGGGGATCAGTGAATTAAATGGGGTC
ATACAAGTATAAAAATTAAAAAAAAAAGACTTCATGCCCAATCTCATATGATGTGGAAGA
ACTGTTAGAGAGACCAACAGGGTAGTGGGTTAGAGATTTCCAGAGTCTTACATTTTCTAG
AGGAGGTATTTAATTTCTTCTCACTCTCTCCAGTGTTGTATTTAGGAATTTCCTGGCAAC
AGAACTCATGGCTTTAATCCCACTAGCTATTGCTTATTGTCCTGGTCCAATTGCCAATTA
CCTGTGTCTTGGAAGAAGTGATTTCTAGGTTCACCATTATGGAAGATTCTTATTCAGAAA
GTCTGCATAGGGCTTATAGCAAGTTATTTATTTTTAAAAGTTCCATAGGTGATTCTGATA
GGCAGTGAGGTTAGGGAGCCACCAGTTATGATGGGAAGTATGGAATGGCAGGTCTTGAAG
ATAACATTGGCCTTTTGAGTGTGACTCGTAGCTGGAAAGTGAGGGAATCTTCAGGACCAT
GCTTTATTTGGGGCTTTGTGCAGTATGGAACAGGGACTTTGAGACCAGGAAAGCAATCTG
ACTTAGGCATGGGAATCAGGCATTTTTGCTTCTGAGGGGCTATTACCAAGGGTTAATAGG
TTTCATCTTCAACAGGATATGACAACAGTGTTAACCAAGAAACTCAAATTACAAATACTA
AAACATGTGATCATATATGTGGTAAGTTTCATTTTCTTTTTCAATCCTCAGGTTCCCTGA
TATGGATTCCTATAACATGCTTTCATCCCCTTTTGTAATGGATATCATATTTGGAAATGC
CTATTTAATACTTGTATTTGCTGCTGGACTGTAAGCCCATGAGGGCACTGTTTATTATTG
AATGTCATCTCTGTTCATCATTGACTGCTCTTTGCTCATCATTGAATCCCCCAGCAAAGT
GCCTAGAACATAATAGTGCTTATGCTTGACACCGGTTATTTTTCATCAAACCTGATTCCT
TCTGTCCTGAACACATAGCCAGGCAATTTTCCAGCCTTCTTTGAGTTGGGTATTATTAAA
TTCTGGCCATTACTTCCAATGTGAGTGGAAGTGACATGTGCAATTTCTATACCTGGCTCA
TAAAACCCTCCCATGTGCAGCCTTTCATGTTGACATTAAATGTGACTTGGGAAGCTATGT
GTTACACAGAGTAAATCACCAGAAGCCTGGATTTCTGAAAAAACTGTGCAGAGCCAAACC
TCTGTCATTTGCAACTCCCACTTGTATTTGTACGAGGCAGTTGGATAAGTGAAAAATAAA
GTACTATTGTGTCAAGTCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

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FIG. 5

MMVDPNGNES SATYFILIGL PGLEEAQ**FWL AFPLCSLYLI AVLGNLTIIY**
IVRTEHSLHE PMY**IFLCMLS GIDILISTSS MPKMLAIFW**F NSTTIQFDAC
LLQM**FAIHSL SGMESTVLLA MAFDRYVAIC** HPLRHATVLT LPRVTK**IGVA**
AVVRGAALMA PLPVFIKQLP FCRSNILSHS YCLHQDVMKL ACDDIR**VNVV**
YGLIVIISAI GLDSLLISFS YLLILKTVLG LTREAQAKA**F GTCVSHVCAV**
FIFYVPFIGL SMVHRFSKRR DSP**LPVILAN IYLLVPPVLN PIVYGV**KTKE
IRQRILRLFH VATHASEP

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FIG. 6A

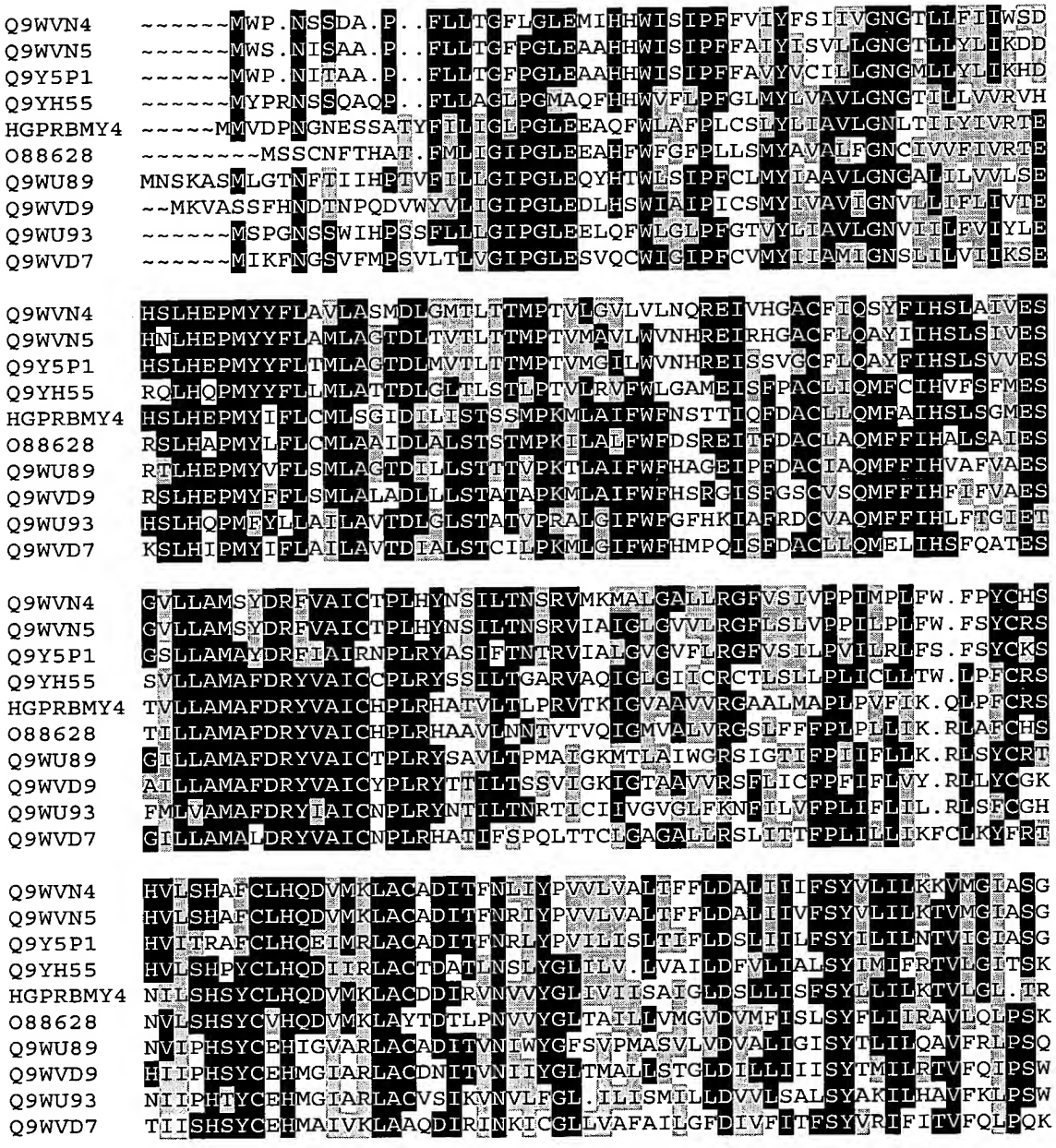
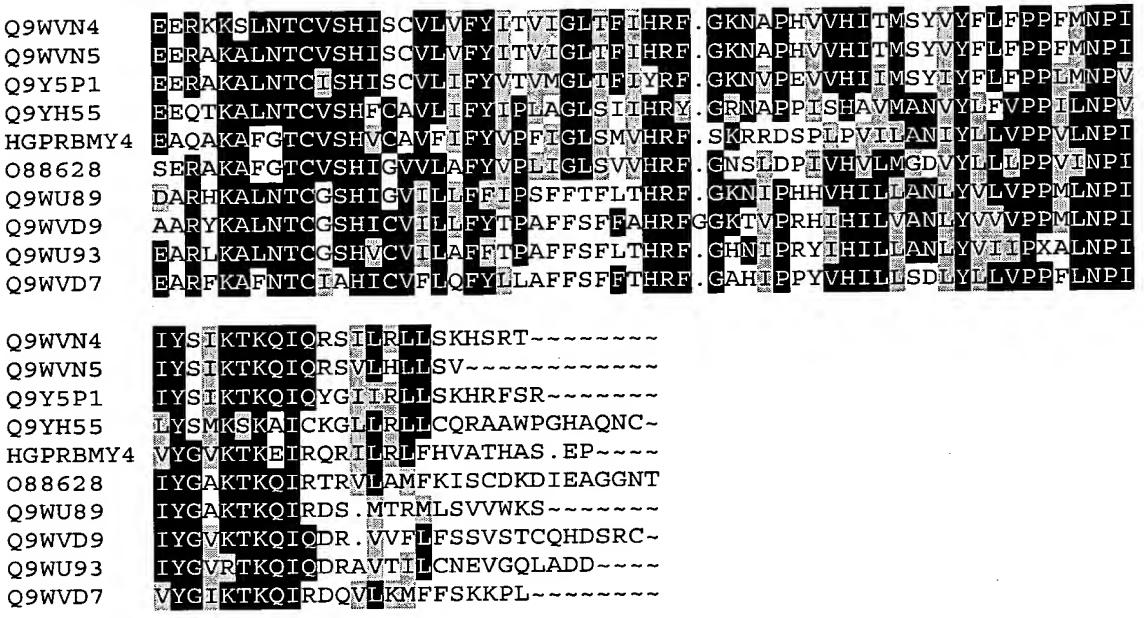

Q9WVN4
Q9WVN5
Q9Y5P1
Q9YH55
HGPRBMY4
O88628
Q9WU89
Q9WVD9
Q9WU93
Q9WVD7

FIG. 6B


Q9WVN4
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Q9Y5P1
Q9YH55
HGPRBMY4
O88628
Q9WU89
Q9WVD9
Q9WU93
Q9WVD7
Q9WVN4
Q9WVN5
Q9Y5P1
Q9YH55
HGPRBMY4
O88628
Q9WU89
Q9WVD9
Q9WU93
Q9WVD7

FIG. 7

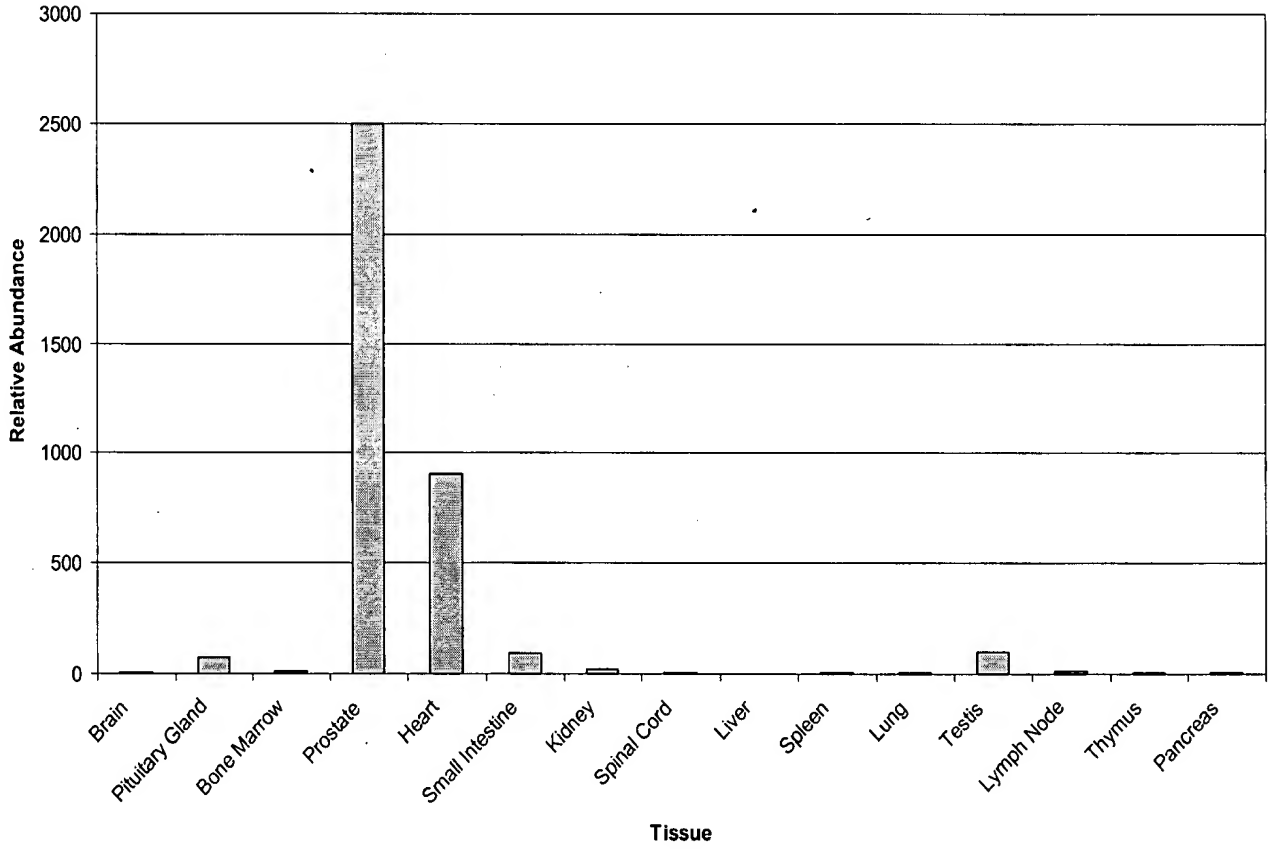

3000
2500
2000
1500
1000
500
0
Relative Abundance
Brain
Pituitary Gland
Bone Marrow
Prostate
Heart
Small Intestine
Kidney
Spinal Cord
Liver
Spleen
Lung
Testis
Lymph Node
Thymus
Pancreas
Tissue

FIG. 8

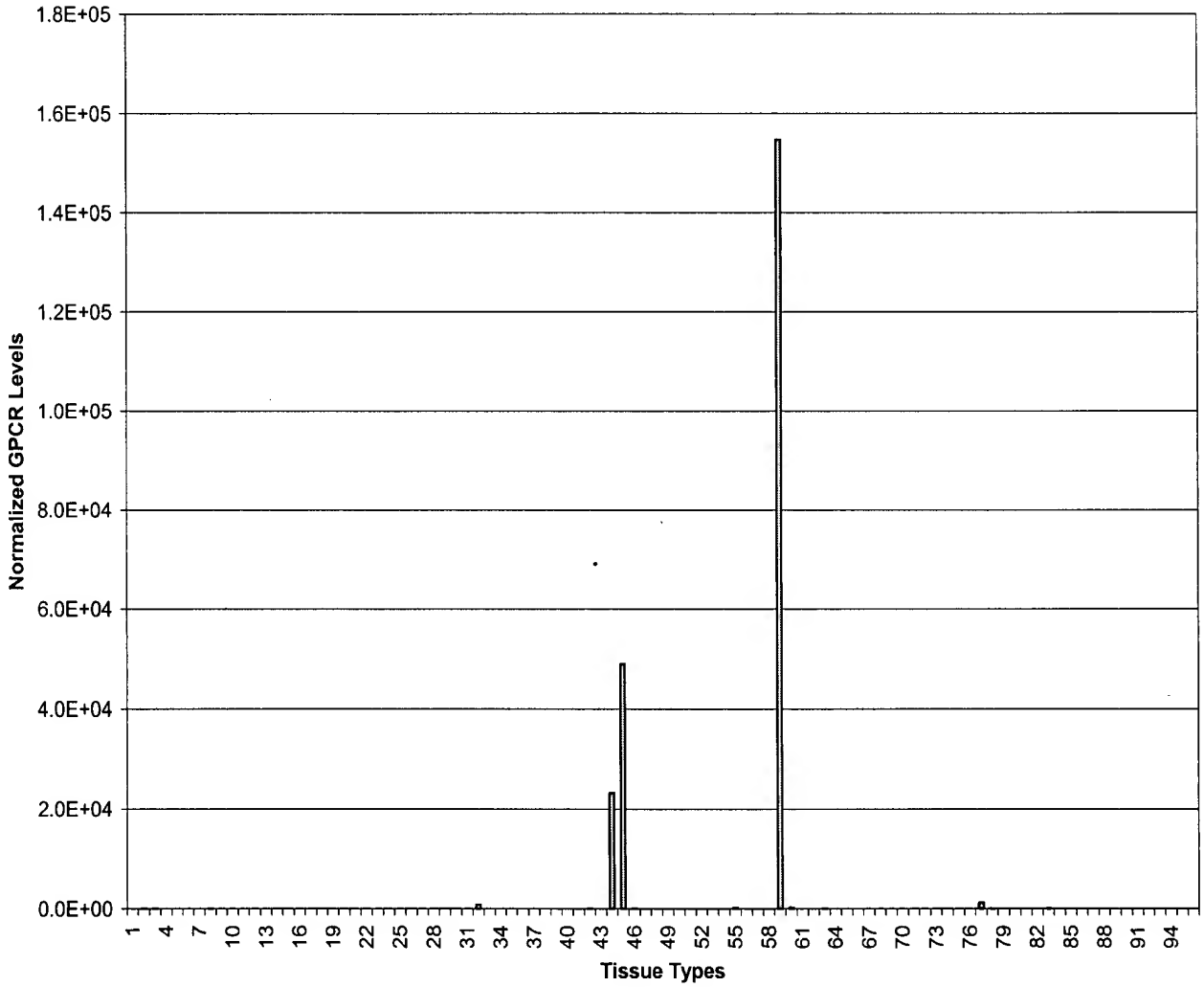

1.8E+05
1.6E+05
1.4E+05
1.2E+05
1.0E+05
8.0E+04
6.0E+04
4.0E+04
2.0E+04
0.0E+00
Normalized GPCR Levels
1
4
7
10
13
16
19
22
25
28
31
34
37
40
43
46
49
52
55
58
61
64
67
70
73
76
79
82
85
88
91
94
Tissue Types

FIG. 9

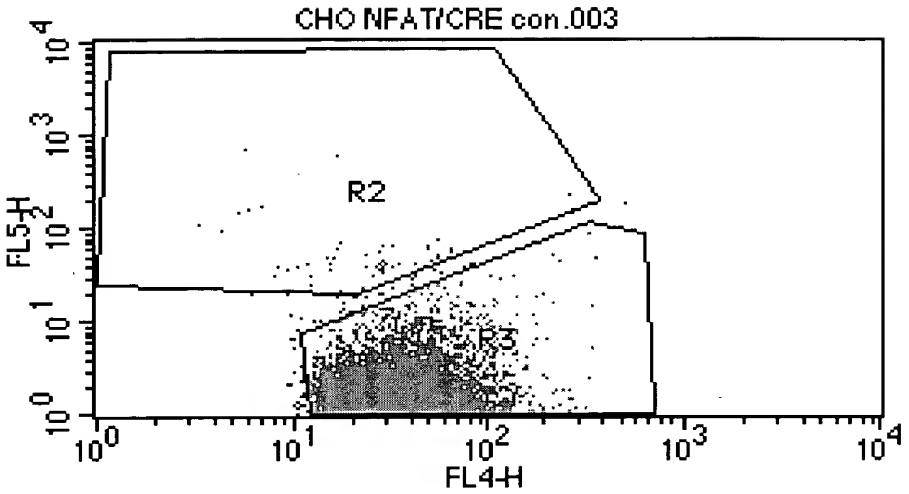
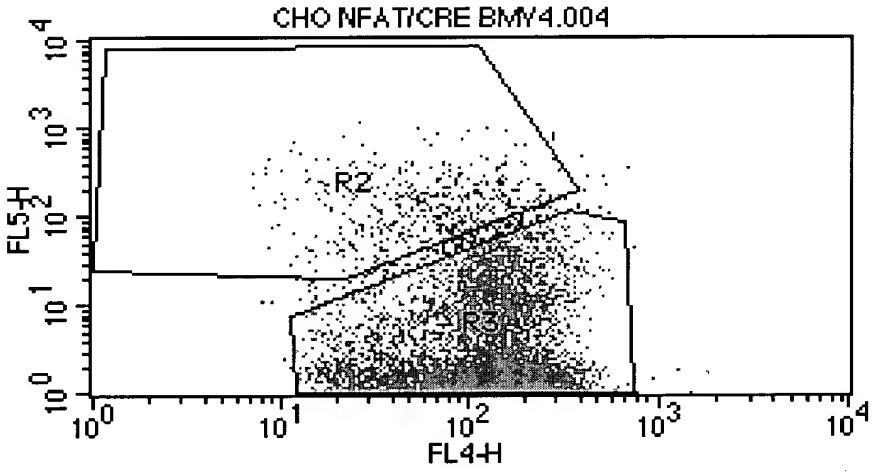


FIG. 10



TOP250 "55455450

FIG. 11

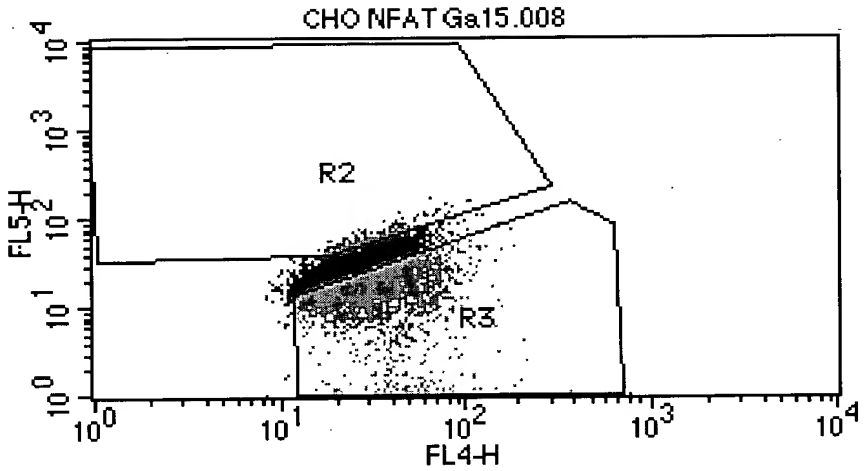


FIG. 12

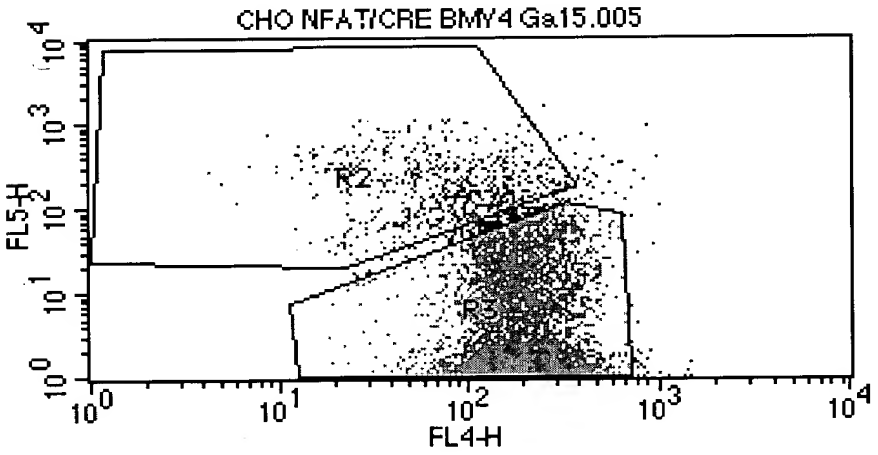


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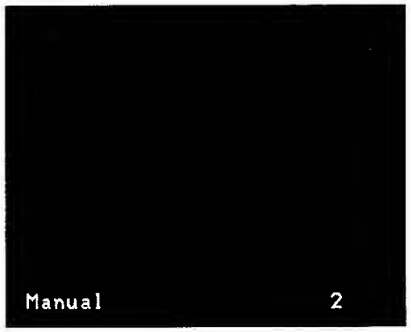
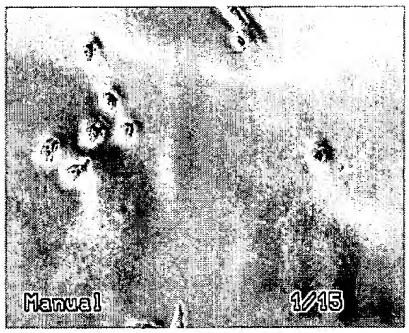
FIG. 13.

a. CHO-NFAT G alpha 15 (Fluorescent vs. Bright Field)





b. CHO-NFAT Galpha 15 HGPRBMY4 (Fluorescent vs. Bright Field)

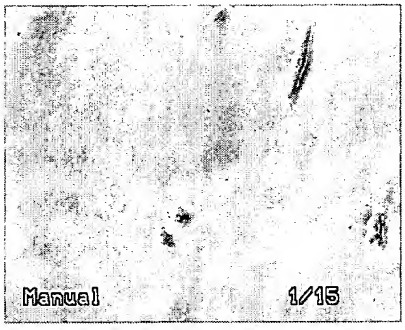


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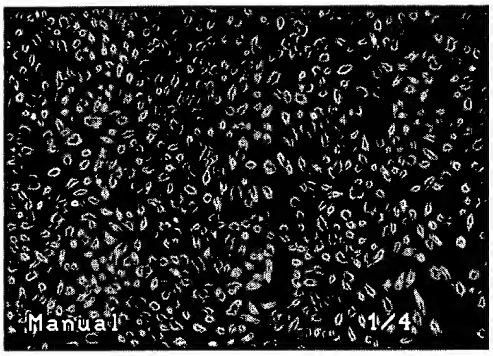
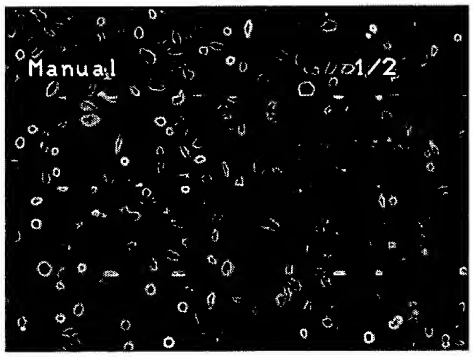
FIG. 14

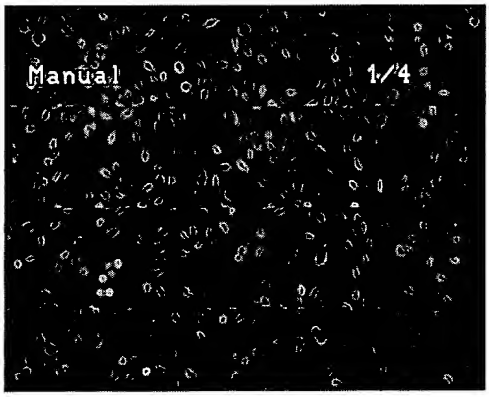
a. CHO-NFAT/ CRE



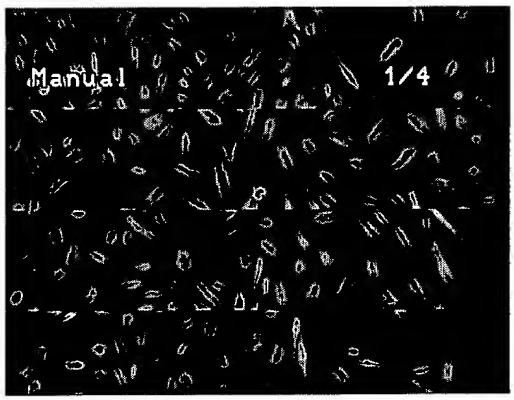
b. CHO-NFAT/CRE + F/T/P



c. CHO-NFAT/CRE oGPCR-Intermediate



d. CHO-NFAT/CRE oGPCR High



TCGGCGAGCGGTATCAGCTCACTCAAAGGCGGTAATACGGTTATCCACAGAATCAGGGGATAACGCAGGAAAGAACATGTGAGCAAAAGGCCAGCAAAAGGCCAGGAACCGTAAAAAGGCCGCGTTGCTGGCGTTTTTCCATAGGCTCCGCCCCCCTGACGAGCATCACAAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAAAGATACCAGGCGTTTCCCCCTGGAAGCTCCCTCGTGCGCTCTCCTGTTCCGACCCTGCCGCTTACCGGATACCTGTCCGCCTTTCTCCCTTCGGGAAGCGTGGCGCTTTCTCATAGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTCGCTCCAAGCTGGGCTGTGTGCACGAACCCCCCGTTCAGCCCGACCGCTGCGCCTTATCCGGTAACTATCGTCTTGAGTCCAACCCGGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATTAGCAGAGCGAGGTATGTAGGCGGTGCTACAGAGTTCTTGAAGTGGTGGCCTAACTACGGCTACACTAGAAGGACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGGAAAAAGAGTTGGTAGCTCTTGATCCGGCAAACAAACCACCGCTGGTAGCGGTGGTTTTTTTGTTTGCAAGCAGCAGATTACGCGCAGAAAAAAAGGATCTCAAGAAGATCCTTTGATCTTTTCTACGGGGTCTGACGCTCAGTGGAACGAAAACTCACGTTAAGGGATTTTGGTCATGAGATTATCAAAAAGGATCTTCACCTAGATCCTTTTAAATTAAAAATGAAGTTTTAAATCAATCTAAAGTATATATGAGTAAACTTGGTCTGACAGTTACCAATGCTTAATCAGTGAGGCACCTATCTCAGCGATCTGTCTATTTCGTTCATCCATAGTTGCCTGACTCCCCGTCGTGTAGATAACTACGATACGGGAGGGCTTACCATCTGGCCCCAGTGCTGCAATGATACCGCGAGACCCACGCTCACCGGCTCCAGATTTATCAGCAATAAACCAGCCAGCCGGAAGGGCCGAGCGCAGAAGTGGTCCTGCAACTTTATCCGCCTCCATCCAGTCTATTAATTGTTGCCGGGAAGCTAGAGTAAGTAGTTCGCCAGTTAATAGTTTGCGCAACGTTGTTGCCATTGCTACAGGCATCGTGGTGTCACGCTCGTCGTTTGGTATGGCTTCATTCAGCTCCGGTTCCCAACGATCAAGGCGAGTTACATGATCCCCCATGTTGTGCAAAAAAGCGGTTAGCTCCTTCGGTCCTCCGATCGTTGTCAGAAGTAAGTTGGCCGCAGTGTTATCACTCATGGTTATGGCAGCACTGCATAATTCTCTTACTGTCATGCCATCCGTAAGATGCTTTTCTGTGACTGGTGAGTACTCAACCAAGTCATTCTGAGAATAGTGTATGCGGCGACCGAGTTGCTCTTGCCCGGCGTCAATACGGGATAATACCGCGCCACATAGCAGAACTTTAAAAGTGCTCATCATTGGAAAACGTTCTTCGGGGCGAAAACTCTCAAGGATCTTACCGCTGTTGAGATCCAGTTCGATGTAACCCACTCGTGCACCCAACTGATCTTCAGCATCTTTTACTTTCACCAGCGTTTCTGGGTGAGCAAAAACAGGAAGGCAAAATGCCGCAAAAAAGGGAATAAGGGCGACACGGAAATGTTGAATACTCATACTCTTCCTTTTTCAATATTATTGAAGCATTTATCAGGGTTATTGTCTCATGAGCGGATACATATTTGAATGTATTTAGAAAAATAAACAAATAGGGGTTCCGCGCACATTTCCCCGAAAAGTGCCACCTGACGTCTAAGAAACCATTATTATCATGACATTAACCTATAAAAATAGGCGTATCACGAGGCCCTTTCGTCTTCAAGAATTCGCCACCATGGGCTGCTCCTTCACCGCCGAGGACAAGGCCGCCGCCGAGCGCAGCAAGATGATCGACAAGAACCTGCAGGAGGACGGCGAGAAGGCCGCCCGCGAGGTGAAGCTGCTGCTGCTGGGCGCCGGCGAGAGCGGCAAGAGCACCATCGTGAAGCAGATGAAGATCATCCACGAGGACGGCTACAGCCTGGAGGAGTGCCTGGAGTTCATCGCCATCATCTACGGCAACACCCTGCAGAGCATCCTGGCCATCGTGCGCGCCATGACCACCCTGAACATCCAGTACGGCGACAGCGCCCGCCAGGACGACGCCCGCAAGCTGATGCACATGGCCGACACCATCGAGGAGGGCACCATGCCCAAGGAGATGGCCGACATCATCCAGCGCCTGTGGAAGGACAGCGGCATCCAGGCCTGCTTCGAGCGCGCCAGCGAGTACCAGCTGAACGACAGCGCCGGCTACTACCTGAGCGACCTGGAGCGCCTGGTGACCCCCGGCTACGTGCCCACCGAGCAGGACGTGCTGCGCAGCCGCGTGAAGACCACCGGCATCATCGAGACCCAGTTCAGCTTCAAGGACCTGAACTTCCGCATGTTCGACGTGGGCGGCCAGCGCAGCGAGCGCAAGAAGTGGATCCACTGCTTCGAGGGCGTGACCGCCCTGATCTTCATCGCCGCCCTGAGCGAGTACGACCAGGTGCTGGTGGAGAGCGACAACGAGAACCGCATGGAGGAGAGCAAGGCCCTGTTCCGCACCATCATCACCTACCCCTGGTTCCAGAACAGCAGCGTGATCCTGTTCCTGAACAAGAAGGACCTGCTGGAGGACAAGATCATGTACAGCCACCTGGTGGACTACTTCCCCGAGTACGACGGCCCCCAGCGCGACGCCCAGGCCGCCCGCGAGTTCATCCTGAAGATGTTCGTGGACCTGAACCCCGACAGCGACAAGATCATCTACAGCCACTTCACCTGCGCCACCGACACCGAGAACATCCGCTTCGTGTTCGCCGCCGTGAAGGACACCATCCTGCAGCTGAACCTGAAGGAGTACAACCTGGTGTAGTCTAGAGGATCCCCGGGTACCGAGCTCGAATTCACTGGCCGTCGTTTTACAACGTCGTGACTGGGAAAACCCTGGCGTTACCCAACTTAATCGCCTTGCAGCACATCCCCCTTTCGCCAGCTGGCGTAATAGCGAAGAGGCCCGCACCGATCGCCCTTCCCAACAGTTGCGCAGCCTGAATGGCGAATGGCGCCTGATGCGGTATTTTCTCCTTACGCATCTGTGCGGTATTTCACACCGCATATGGTGCACTCTCAGTACAATCTGCTCTGATGCCGCATAGTTAAGCCAGCCCCGACACCCGCCAACACCCGCTGACGCGCCCTGACGGGCTTGTCTGCTCCCGGCATCCGCTTACAGACAAGCTGTGACCGTCTCCGGGAGCTGCATGTGTCAGAGGTTTTCACCGTCATCACCGAAACGCGCGAGGCAGCTGCGGTAAAGCTCATCAGCGTGGTCGTGAAGCGATTCACAGATGTCTGCCTGTTCATCCGCGTCCAGCTCGTTGAGTTTCTCCAGAAGCGTTAATGTCTGGCTTCTGATAAAGCGGGCCATGTTAAGGGCGGTTTTTTCCTGTTTGGTCACTTGATGCCTCCGTGTAAGGGGGATTTCTGTTCATGGGGGTAATGATACCGATGAAACGAGAGAGGATGCTCACGATACGGGTTACTGATGATGAACATGCCCGGTTACTGGAACGTTGTGAGGGTAAACAACTGGCGGTATGGATGCGGCGGGACCAGAGAAAAATCACTCAGGGTCAATGCCAGCGCTTCGTTAATACAGATGTAGGTGTTCCACAGGGTAGCCAGCAGCATCCTGCGATGCAGATCCGGAACATAATGGTGCAGGGCGCTGACTTCCGCGTTTCCAGACTTTACGAAACACGGAAACCGAAGACCATTCATGTTGTTGCTCAGGTCGCAGACGTTTTGCAGCAGCAGTCGCTTCACGTTCGCTCGCGTATCGGTGATTCATTCTGCTAACCAGTAAGGCAACCCCGCCAGCCTAGCCGGGTCCTCAACGACAGGAGCACGATCATGCGCACCCGTGGCCAGGACCCAACGCTGCCCGAGATGCGCCGCGTGCGGCTGCTGGAGATGGCGGACGCGATGGATATGTTCTGCCAAGGGTTGGTTTGCGCATTCACAGTTCTCCGCAAGAATTGATTGGCTCCAATTCTTGGAGTGGTGAATCCGTTAGCGAGGTGCCGCCGGCTTCCATTCAGGTCGAGGTGGCCCGGCTCCATGCACCGCGACGCAACGCGGGGAGGCAGACAAGGTATAGGGCGGCGCCTACAATCCATGCCAACCCGTTCCATGTGCTCGCCGAGGCGGCATAAATCGCCGTGACGATCAGCGGTCCAGTGATCGAAGTTAGGCTGGTAAGAGCCGCGAGCGATCCTTGAAGCTGTCCCTGATGGTCGTCATCTACCTGCCTGGACAGCATGGCCTGCAACGCGGGCATCCCGATGCCGCCGGAAGCGAGAAGAATCATAATGGGGAAGGCCATCCAGCCTCGCGTCGCGAACGCCAGCAAGACGTAGCCCAGCGCGTCGGCCGCCATGCCGGCGATAATGGCCTGCTTCTCGCCGAAACGTTTGGTGGCGGGACCAGTGACGAAGGCTTGAGCGAGGGCGTGCAAGATTCCGAATACCGCAAGCGACAGGCCGATCATCGTCGCGCTCCAGCGAAAGCGGTCCTCGCCGAAAATGACCCAGAGCGCTGCCGGCACCTGTCCTACGAGTTGCATGATAAAGAAGACAGTCATAAGTGCGGCGACGATAGTCATGCCCCGCGCCCACCGGAAGGAGCTGACTGGGTTGAAGGCTCTCAAGGGCATCGGTCGAGATCCCGGTGCCTAATGAGTGAGCTAACTTACATTAATTGCGTTGCGCTCACTGCCCGCTTTCCAGTCGGGAAACCTGTCGTGCCAGCTGCATTAATGAATCGGCCAACGCGCGGGGAGAGGCGGTTTGCGTATTGGGCGCTCTTCCGCTTCCTCGCTCACTGACTCGCTGCGCTCGGTCGTTCGGCTG

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